

Access DB#

74285

SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 8/25/02
Art Unit: 1635 Phone Number 30 6-5220 Serial Number: 09/522,278
Mail Box and Bldg/Room Location: 11D03 Results Format Preferred (circle): PAPER DISK E-MAIL

11e12
If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Delivery of Substances to Cells

Inventors (please provide full names): O'Hare et al.

Earliest Priority Filing Date: 2/14/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search Sig ID No 12

Sig limited to 50 AA

Unlimited search

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Interference + Regular
Data Bases
Thanks.

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>8/28/02</u>	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>✓</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: August 28, 2002, 12:23:41 : Search time 30.25 seconds

(Without alignments)
1721.371 Million cell updates/sec

Title: US-09-522-278b-12

Perfect score: 1561
Sequence: 1 MTRSRVSKSGPREVPRDEYE.....PTERRAPARSASRRPRVPE 301

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

SPREMBL_19:*

- 1: SP_archaea:*
- 2: SP_bacteria:*
- 3: SP_fungi:*
- 4: SP_human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_rodent:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_virus:*
- 16: SP_bacterioph:*
- 17: SP_archaeo:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104.5	65.0	300	12 P89468	P89468 herpes simp
2	270.5	17.3	304	12 Q39253	Q39253 equine herp
3	228	14.6	301	12 Q9E306	Q9E306 cercopithec
4	210	13.5	249	12 Q69318	Q69318 marek's dis
5	210	13.5	249	12 Q9E6M7	Q9E6M7 turkey herp
6	207	13.3	241	12 Q89247	Q89247 gallid herp
7	198	12.7	283	12 Q9DH2	Q9DH2 meleagrid h
8	168.5	10.8	388	12 Q9NY42	Q9NY42 homo saplen
9	168.5	10.8	441	4 Q75685	Q75685 homo saplen
10	153	9.8	252	12 Q9DMG9	Q9DMG9 rat cytoleg
11	149.5	9.6	956	4 Q9UQ35	Q9UQ35 homo saplen
12	149.5	9.6	2752	4 Q9UQ35	Q9UQ35 herpes simp
13	149.5	9.6	3122	12 P89459	P89459 gallid herp
14	148	9.5	266	12 Q56868	Q56868 delnococtus
15	146.5	9.4	395	16 Q9RVT4	Q9RVT4 delnococtus
16	146.5	9.4	1343	4 Q9H7M4	Q9H7M4 homo saplen

17	146	9.4	839	16 Q9RX57	Q9RX57 delnococtus
18	146	9.4	1262	4 Q9UQ40	Q9UQ40 homo saplen
19	144	9.2	1037	16 Q9AC25	Q9AC25 caulobacter
20	144	9.2	1201	10 Q9CGS1	Q9CGS1 arabidopsis
21	143.5	9.2	889	4 Q9UL51	Q9UL51 homo saplen
22	143.5	9.2	1154	4 Q9P2P0	Q9P2P0 homo saplen
23	142	9.1	1249	5 Q9M8C4	Q9M8C4 typanosoma
24	140.5	9.0	1265	3 Q9S970	Q9S970 pneumocysti
25	140.5	9.0	1592	3 Q9P6T1	Q9P6T1 neurospora
26	140	9.0	1132	16 Q9RRC7	Q9RRC7 delnococtus
27	139.5	8.9	932	5 Q93562	Q93562 caenorhabdl
28	139	8.9	438	16 Q9A2M5	Q9A2M5 caulobacter
29	138.5	8.9	1312	4 Q9NR59	Q9NR59 homo saplen
30	137	8.8	590	2 Q9S205	Q9S205 streptomyc
31	137	8.8	797	2 Q9RKS9	Q9RKS9 streptomyc
32	137	8.8	835	2 Q9K3E2	Q9K3E2 streptomyc
33	137	8.8	1069	12 Q69140	Q69140 human herpe
34	136.5	8.7	694	6 Q9GK7	Q9GK7 oryctolagus
35	136.5	8.7	889	4 Q9US82	Q9US82 homo saplen
36	136.5	8.7	1320	11 Q08784	Q08784 homo saplen
37	136	8.7	212	11 Q70446	Q70446 mus musculu
38	136	8.7	436	4 Q9S01	Q9S01 homo saplen
39	136	8.7	2936	5 Q9NKP7	Q9NKP7 leishmania
40	135.5	8.7	612	2 Q92614	Q92614 streptomyc
41	135.5	8.7	1175	6 Q9TV66	Q9TV66 oryctolagus
42	134	8.6	667	11 Q9RID9	Q9RID9 mus musculu
43	134	8.6	721	4 Q9E648	Q9E648 homo saplen
44	134	8.6	737	11 Q9WVF3	Q9WVF3 mus musculu
45	134	8.6	806	11 Q9WVF4	Q9WVF4 mus musculu

ALIGNMENTS

RESULT 1

ID P89468 PRELIMINARY: PRT: 300 AA.

AC P89468: 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE TEGUMENT PROTEIN.

GN U149.

OS Herpes simplex virus (type 2).

OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:

OC Alphaherpesvirinae: Simplexvirus.

OK NCBI_TaxID=10310;

RN [1]

RP SEQUENCE FROM N.A.

RP STRAIN=HG52:

RX MEDLINE=87111457; PubMed=3027242;

RA McGeoch D.J., Moss H.W., McNab D., Frame M.C.:

RT "DNA sequence and genetic content of the HindIII 1 region in the short

RT unique component of the herpes simplex virus type 2 genome:

RT Identification of the gene encoding glycoprotein G, and evolutionary

RT comparisons.";

RL J. Gen. Virol. 68:19-38(1987).

RL [2]

RP SEQUENCE FROM N.A.

RP STRAIN=HG52:

RX MEDLINE=90278430; PubMed=2161906;

RA Everett R., Fenwick M.:

RT "Comparative DNA sequence analysis of the host shut-off genes of

RT different strains of herpes simplex virus: type 2 strain HG52 encodes

RT a truncated U11 product."

RL J. Gen. Virol. 71:1387-1390(1990).

RL [3]

RP SEQUENCE FROM N.A.

RP STRAIN=HG52:

RX MEDLINE=92113549; PubMed=1662697;

RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.:

RT "Comparative sequence analysis of the long repeat regions and

RT adjoining parts of the long unique regions in the genomes of herpes